cycle) on optimal LeMaster Richards's minimal media supplemented with carbon source 2-13C-glycerol alone or in combination with 13C-formate to enhance labeling at carbon positions bearing protons that are useful for NMR studies. Experimental results showed that the strains produced specific ribose and nucleotide labels that were readily predicted. These labels will enable us to study the structure, function and dynamics of higher size RNA molecules using NMR that would have been otherwise difficult if the commercially available uniformly labeled or unlabeled ribonucleotides were utilized.

1303-Pos Board B213
Characterization of ps-Ms Dynamics in the TAR Apical Loop by NMR
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The transactivation response element (TAR) is located at the 5′ end of the HIV-1 genome and regulates the transcription elongation step of viral RNA. The TAR stem-loop binds the HIV viral transactivator protein (Tat) and human positive transcription elongation factor b (P-TEFb), leading to productive transcription of the HIV genome. The formation of the TAR/Tat/P-TEFb ribonucleoprotein complex remains poorly understood from a structural and dynamical standpoint. To better understand its formation, we have studied the structural and dynamic features of free TAR to elucidate motions in both the bulge and apical loop that may be important for adaptive recognition of protein targets.
A combination of nuclear magnetic resonance (NMR) relaxation techniques, including ^{13}C relaxation (R_1, R_2) and ^{13}C $R_{1\rho}$ relaxation dispersion, were used to characterize local and global dynamics at the ps-ns timescale and to site-specifically quantify slow motions on the us-ms timescale, respectively. ^{13}C $R_{1\rho}$ relaxation dispersion reveals the presence of us-ms exchange in the loop caused by the existence of ''invisible'' excited states. Full characterization of these excited states may give insight into the recognition of Tat and P-TEFb by TAR. In general, our results reveal that the apical loop and bulge undergo complex dynamics at multiple timescales that are likely important for adaptive recognition.

1304-Pos Board B214
Site-Pecific Fluorescnce Dynamics in an RNA 'THERMOMETER' Reveals the Mechanism of Temperature-Sensitive Translation
Mamata Kombrabail, Suman Paul, Basukthar J. Rao,
Guruswamy Krishnamoorthy.
The ROSE (**R**epression **O**f heat **S**hock gene **E**xpression) element of mRNA present in the 5'-UTR of small heat-shock genes in many Gram-negative bacteria is known to function as a 'RNA thermometer' by controlling protein translation in a temperature range of 30 - 42° C where the translation is blocked till 30°C and allowed at 42°C and beyond, perhaps due to an unfolding transition of the ROSE hair-pin motif.
In this work, we have used site-specific fluorescence labeling and pico-second time-domain fluorescence spectroscopy to unravel the mechanism. The 'ROSE RNA' was site-specially labeled with 2-aminopurine (2-AP), a fluorescent analog of adenine. Observables such as fluorescence lifetime, fluorescence anisotropy decay kinetics and dynamic fluorescence quenching revealed properties such as the level of base stacking, rotational motion of the bases, segmental dynamics of the backbone and the level of exposure of base to solvent. As expected, all read-outs of 2-AP residue that were studied showed remarkable position-dependence/sensitivity in the RNA sequence at 25°C. The striking result was the persistence of the same position-dependence of the parameters even at 45°C albeit at a measurably reduced levels. However the same position-dependence was nearly 'wiped out' in the presence of urea where all intra-molecular interactions in RNA are undone. These observations have prompted us to revise the existing model of ROSE RNA action: we now suggest that unlike proposed earlier, the thermometer action of ROSE emanates not from its unfolding structural transition between 25 and 45°C, but rather from its propensity to enhance structural dynamics without ''melting'' the structure. We hypothesize that either the enhanced dynamics of the structure it self or its full melting due to an extrinsic factor (perhaps a protein interaction) might be the basis of its thermometer action.

1305-Pos Board B215
Revealing the Energy Landscapes of Ribosome Function
Paul C. Whitford, Christian M.T. Spahn, Scott C. Blanchard,
Jose' N. Onuchic, Karissa Y. Sanbonmatsu.
The ribosome is a massive ribonucleoprotein complex (~2.4 MDa) that harnesses large-scale structural fluctuations to produce unidirectional protein synthesis. We address the relationship between ribosome energetics, structural fluctuations and biological function via all-atom molecular dynamics simulations. Specifically, we utilized large-scale explicit-solvent simulations (3.2 million atoms), in addition to models that employ simplified energetics (~150,000 atoms) to describe the microsecond to millisecond processes associated with transfer RNA molecules as they enter, and move through, the ribosome. By simulating ribosomal hybrid-state formation, we have identified common physical principles that guide multiple rearrangements during ribosome function. This work demonstrates that the configurational entropy contributes significantly to the landscape, which has implications for fidelity and efficiency of ribosome function.

1306-Pos Board B216
A Coarse Grain RNA Model for Exploration of RNA Conformational Space
Anthony M. Mustoe, Hashim M. Al-Hashimi, Charles L. Brooks III.
Several recent studies have suggested that RNA three-dimensional structure and dynamics are highly restricted to a small set of allowed conformations by topological constraints that are encoded at the secondary structure level. We have developed a coarse-grained model of RNA implemented within the CHARMM molecular dynamics package that allows us to further characterize the nature of RNA topological constraints. In this coarse grain model, each residue is represented using three pseudo-atoms for the phosphate, sugar, and base moieties respectively. Secondary structure is specified by modeling bonds between paired bases and parameterizing these regions to adopt A-form helical structure. All non-base paired residues are modeled without torsional potentials or attractive non-bonded forces, preserving only connectivity and repulsive steric terms. Thus, the energy landscape between different helical orientations is effectively flat, allowing efficient exploration of topologically allowed conformations.
We benchmark our simulations using results from prior NMR and bioinformatics studies of two-way helix junctions. Moreover, simulations starting from a linear chain of the 76 residue tRNA-Phe molecule show that our model is able to sample the native conformation with minimal computational effort. We also show that the size of the conformational ensemble is reduced by over an order of magnitude when a limited set of three non-crystallographically determined tertiary contacts are used as restraints. In fact, the mean all phosphate RMSD over an ensemble of 100,000 structures has a value of 10 Å. We also present preliminary results of simulations done on RNAs with greater than 200 residues. These results suggest topological constraints alone, coupled with a few important tertiary contacts for larger RNAs, are enough to significantly constrain the available conformational ensemble and suggest a new approach to RNA structure prediction that is applicable to very large RNAs.

1307-Pos Board B217
Computing the Conformational Entropy for RNA Folds
Liang Liu, Shi-jie Chen.
We develop a polymer physics-based method to compute the conformational entropy for RNA tertiary folds, namely, conformations consisting of multiple helices connected through cross-linked loops. The theory is based on a virtual bond conformational model for the nucleotide chain. A key issue in the calculation of the entropy is how to treat the excluded volume interactions. The weak excluded volume interference between the different loops leads to the decomposition of the whole structure into a number of three-body building blocks, each consisting of a loop and two helices connected to the two ends of the loop. The simple construct of the three-body system allows an accurate computation for the conformational entropy for each building block. The assembly of the building blocks gives the entropy of the whole structure. This approach enables treatment of molten globule-like folds partially unfolded tertiary structures for RNAs. Extensive tests against experiments and exact computer enumerations indicate that the method can give accurate results for the entropy. The method developed here provides a solid first step toward a systematic development of a theory for the entropy and free energy landscape for complex tertiary folds for RNAs and proteins.(Liu,L. and Chen,S.-J., J. Chem. Phys, 132, 235104; doi:10.1063/1.3447385).

1308-Pos Board B218
Fibonacci Primes and Topological Biomolecular Mechanics
Okan Gurel, Demet Gurel.
Leonardo Fibonacci (c.1170-c.1250) in his book *Liber Abaci* (1202) presented two sequences: Fibonacci (Arithmetic) Sequence, Fa, ([1], p.260), and Fibonacci (Geometric) Sequence, Fg, ([1], p.404). We show that when Fg {Congruence (mod Fg6)} prime factorized, reveals 11 primes, which we named